

SEQUENCE LISTING



<110> Council of Scientific and Industrial Research

<120> Method for detection of human spinocerebellar ataxia 2  
gene variants

<130> US 443

<140> 09/707919

<141> 2000-11-08

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for  
amplification of SCA2 gene region containing one  
or more polymorphic sites

<220>

<400> 1

ctccgcctca gactgttttg gtag

24

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for  
amplification of SCA2 gene region containing one  
or more polymorphic sites

<400> 2

gtggccgagg acgaggagac

20

<210> 3

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for  
detection of allelic variants of SCA2 gene

<400> 3

ctcggcgggc ctccccgcc cttcgtcgtc c

31

RECEIVED  
FEB 12 2003  
TECH CENTER 160012900

<210> 4  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele  
specific primer for detection of allelic variants  
of SCA2 gene

<400> 4  
ctcggcgggc ctccccgccc cttcgtcgtc g

31

<210> 5  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele  
specific primer for detection of allelic variants  
of SCA2 gene

<400> 5  
cctccccgcc cttcgtcgt c

21

<210> 6  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele  
specific primer for detection of allelic variants  
of SCA2 gene

<400> 6  
cgccaaccgc cgctccccg ctcggcgccc gc

32

<210> 7  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele  
specific primer for detection of allelic variants  
of SCA2 gene

<400> 7  
cgccaaccgc cgctccccg ctcggcgccc gt

32

<210> 8  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele  
specific probe for detection of allelic variants  
of SCA2 gene

<400> 8  
gcgcctcccc gctcggcgcc cg

22

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele specific  
probe for detection of allelic variants of SCA2  
gen

<400> 9  
ccccttcgtc gtcctccttc tccccct

27

<210> 10  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele specific  
probe for detection of allelic variants of SCA2  
genE

<400> 10  
ccccttcgtc gtcgtccttc tccccct

27

<210> 11  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele specific  
probe for detection of allelic variants of SCA2  
gene

<400> 11  
cgctcggcgc ccgcggtcc ccgccgc

27

<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Allele specific  
probe for detection of allelic variants of SCA2  
gene

<400> 12  
cgctcggcgc ccgtgcgtcc ccgccgc

27

<210> 13  
<211> 459  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Description of  
Artificial derived nucleotide sequence of allelic  
variant of SCA2 gene

<400> 13  
ctccgcctca gactgttttg gtagcaacgg caacggcggc ggcgcgtttc ggcccggctc 60  
ccggcggttc cttggtctcg gcgggcctcc ccgcccttc gtcgtctcc ttctccccct 120  
cgccagcccg ggcgccctc cgccgcgcc aaccgcgcc tccccgtcg gcgcccgcgc 180  
gtccccgcg cgttcggcg tctccttggc gcgcccggct cccggtgtc cccgcccggc 240  
gtgcgagccg gtgtatggc cctcaccat gtcgtgaag cccagcagc agcagcagca 300  
gcagcagcaa cagcagcagc agcaacagca gcagcagcag cagcagcagc cgcgcccgc 360  
ggctgccaat gtccgcaagc ccggcggcag cggccttcta gcgtcgcccg ccgcccgcgc 420  
ttcgccgtcc tcgtcctcg tctcctcgtc ctcgccac 459

<210> 14  
<211> 106  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Flanking sequence Human ataxin-2 gene

<400> 14  
ctccgcctca gactgttttg gtagcaacgg caacggcggc ggcgcgtttc ggcccggctc 60  
ccggcggttc cttggtctcg gcgggcctcc ccgcccttc gtcgtc 106

<210> 15  
<211> 169  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Flanking sequence Human ataxin-2 gene

<400>  
tccttctccc cctcgccagc ccggggcgccc ctccggccgc gccaaaccgc gcctccccgc 60  
tcggcgcccg tgcgtccccg ccgcgttccg gcgtctcctt ggcgcgcccg gctcccggct 120

gtccccgccc ggcgtgagag ccggtgtatg ggccccctcac catgtcgct 169

<210> 16  
<211> 183  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Flanking sequence Human ataxin-2 gene

<400> 16  
gaagccccag cagcagcagc agcagcagca gcaacagcag cagcagcaac agcagcagca 60  
gcagcagcag cagccgcccgc ccgcggtctgc caatgtccgc aagccccggcg gcagcggcct 120  
tctagcgctg cccgcgcgcg cgccttcgcc gtccctcgcc tcggtctcct cgtcctcggc 180  
cac 183

<210> 17  
<211> 177  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Flanking sequence Human ataxin-2 gene

<400> 17  
ctccgcctca gactgttttg gtagcaacgg caacggcggc ggcgcgtttc ggccccggctc 60  
ccggcgggctc cttggtctcg gcgggcctcc ccgccccctc gtcgtcgctc ttctccccct 120  
cgccagcccc ggcgccccctc cggccgcgcc aaccgcgcgc tccccgctcg gcgcccc 177

<210> 18  
<211> 98  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Flanking sequence Human ataxin-2 gene

<400> 18  
gcgtccccgc cgcgttcagg cgtctccttg gcgcgcccgg ctcccggctg tccccgcccc 60  
gcgtgcgagc cgggtgtatg gccctcacc atgtcgct 98

<210> 19  
<211> 1312  
<212> PRT  
<213> Homo sapiens

<400> 19

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu  
1 5 10 15

Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln  
20 25 30

Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly  
35 40 45

Pro Tyr Pro Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro  
 50 55 60

Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn  
 65 70 75 80

Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly  
 85 90 95

Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala  
 100 105 110

Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly  
 115 120 125

Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala  
 130 135 140

Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr  
 145 150 155 160

Met Ser Leu Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln  
 165 170 175

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala  
 180 185 190

Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala  
 195 200 205

Ala Ala Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr  
 210 215 220

Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly  
 225 230 235 240

Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile  
 245 250 255

Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr  
 260 265 270

Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile  
 275 280 285

Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu  
 290 295 300

Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg  
 305 310 315 320

Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val  
 325 330 335

Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe  
 340 345 350

Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys  
 355 360 365  
 Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu  
 370 375 380  
 Glu Ala Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met  
 385 390 395 400  
 Phe Arg Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser  
 405 410 415  
 Ser Leu Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu  
 420 425 430  
 Phe Leu Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu  
 435 440 445  
 Ser Ser Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg  
 450 455 460  
 Ser Glu Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg  
 465 470 475 480  
 Glu Gly His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly  
 485 490 495  
 Gln Arg Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser  
 500 505 510  
 Pro Arg Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr  
 515 520 525  
 Ser His Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val  
 530 535 540  
 Val Asn Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser  
 545 550 555 560  
 Arg Pro Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg  
 565 570 575  
 Ala Ala Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser  
 580 585 590  
 Arg Pro Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser  
 595 600 605  
 Thr Met Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro  
 610 615 620  
 Lys Ala Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly  
 625 630 635 640  
 Ser Ile Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu  
 645 650 655

Ala	Ala	Thr	Pro	Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr	Trp	660	665	670	
Ser	Ser	Val	Val	Ser	Gly	Val	Pro	Arg	Leu	Ser	Pro	Lys	Thr	His	Arg	675	680	685	
Pro	Arg	Ser	Pro	Arg	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Pro	Ser	Gly	Pro	690	695	700	
Val	Leu	Ala	Ser	Pro	Gln	Ala	Gly	Ile	Ile	Pro	Thr	Glu	Ala	Val	Ala	705	710	715	720
Met	Pro	Ile	Pro	Ala	Ala	Ser	Pro	Thr	Pro	Ala	Ser	Pro	Ala	Ser	Asn	725	730	735	
Arg	Ala	Val	Thr	Pro	Ser	Ser	Glu	Ala	Lys	Asp	Ser	Arg	Leu	Gln	Asp	740	745	750	
Gln	Arg	Gln	Asn	Ser	Pro	Ala	Gly	Asn	Lys	Glu	Asn	Ile	Lys	Pro	Asn	755	760	765	
Glu	Thr	Ser	Pro	Ser	Phe	Ser	Lys	Ala	Glu	Asn	Lys	Gly	Ile	Ser	Pro	770	775	780	
Val	Val	Ser	Glu	His	Arg	Lys	Gln	Ile	Asp	Asp	Leu	Lys	Lys	Phe	Lys	785	790	795	800
Asn	Asp	Phe	Arg	Leu	Gln	Pro	Ser	Ser	Thr	Ser	Glu	Ser	Met	Asp	Gln	805	810	815	
Leu	Leu	Asn	Lys	Asn	Arg	Glu	Gly	Glu	Lys	Ser	Arg	Asp	Leu	Ile	Lys	820	825	830	
Asp	Lys	Ile	Glu	Pro	Ser	Ala	Lys	Asp	Ser	Phe	Ile	Glu	Asn	Ser	Ser	835	840	845	
Ser	Asn	Cys	Thr	Ser	Gly	Ser	Ser	Lys	Pro	Asn	Ser	Pro	Ser	Ile	Ser	850	855	860	
Pro	Ser	Ile	Leu	Ser	Asn	Thr	Glu	His	Lys	Arg	Gly	Pro	Glu	Val	Thr	865	870	875	880
Ser	Gln	Gly	Val	Gln	Thr	Ser	Ser	Pro	Ala	Cys	Lys	Gln	Glu	Lys	Asp	885	890	895	
Asp	Lys	Glu	Glu	Lys	Lys	Asp	Ala	Ala	Glu	Gln	Val	Arg	Lys	Ser	Thr	900	905	910	
Leu	Asn	Pro	Asn	Ala	Lys	Glu	Phe	Asn	Pro	Arg	Ser	Phe	Ser	Gln	Pro	915	920	925	
Lys	Pro	Ser	Thr	Thr	Pro	Thr	Ser	Pro	Arg	Pro	Gln	Ala	Gln	Pro	Ser	930	935	940	
Pro	Ser	Met	Val	Gly	His	Gln	Gln	Pro	Thr	Pro	Val	Tyr	Thr	Gln	Pro	945	950	955	960



Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly	965	970	975
Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln	980	985	990
Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp	995	1000	1005
Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly	1010	1015	1020
Pro Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val	1025	1030	1035
Ala Tyr Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His	1040	1045	1050
Val Pro His Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val	1055	1060	1065
Ile Gln Gly Asn Ala Arg Met Met Ala Pro Pro Thr His Ala Gln	1070	1075	1080
Pro Gly Leu Val Ser Ser Ser Ala Thr Gln Tyr Gly Ala His Glu	1085	1090	1095
Gln Thr His Ala Met Tyr Ala Cys Pro Lys Leu Pro Tyr Asn Lys	1100	1105	1110
Glu Thr Ser Pro Ser Phe Tyr Phe Ala Ile Ser Thr Gly Ser Leu	1115	1120	1125
Ala Gln Gln Tyr Ala His Pro Asn Ala Thr Leu His Pro His Thr	1130	1135	1140
Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly Gln Gln Gln Ser	1145	1150	1155
Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val Gln His His	1160	1165	1170
Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro Gln Gln	1175	1180	1185
Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro Ser	1190	1195	1200
Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn Ser Phe Pro	1205	1210	1215
Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln	1220	1225	1230
Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala	1235	1240	1245

His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala  
1250 1255 1260

Pro Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala  
1265 1270 1275

Ala Leu Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr  
1280 1285 1290

Ala His Phe Pro Tyr Met Thr His Pro Ser Val Gln Ala His His  
1295 1300 1305

Gln Gln Gln Leu  
1310

<210> 20

<211> 4481

<212> DNA

<213> Homo sapiens

<400> 20

```
acccccgaga aagcaaccca gcgcgccgcc cgctcctcac gtgtccctcc cggccccggg 60
gccacctcac gttctgcttc cgtctgaccc ctccgacttc cggtaaagag tccctatccg 120
cacctccgct cccaccgcgc gcctcggcgc gcccgccctc cgatgcgctc agcggccgca 180
gctcctcgga gtcccgcggt ggccaccgag tctcgccgct tcgccgcagc caggtggccc 240
gggtggcgct cgctccagcg gccggcgcgg cggagcgggc ggggcggcgg tggcgcggcc 300
ccgggaccgt atccctccgc cgccctccc ccgcccggcc ccggccccc tccctcccgg 360
cagagctcgc ctccctccgc ctccagactgt tttggtagca acggcaacgg cggcggcgcg 420
tttcggcccc gctccggcg gctccttggc ctccggcgggc ctcccgcgcc ctccgctcgc 480
gtccttctcc cctcgcag ccggggcgcc cctccggcgc cgccaaccg cgcctccccg 540
ctcggcgccc gtgcgtcccc gccggttcc ggcgctcct tggcgcgccc ggctcccggc 600
tgtccccgcc cggcgtgcga gccggtgtat gggccctca ccatgtcgct gaagccccag 660
cagcagcagc agcagcagca gcaacagcag cagcagcaac agcagcagca gcagcagcag 720
cagccgcgcg ccggcgctgc caatgtccgc aagcccggcg gcagcgccct tctagcgtcg 780
cccgcgcgcg cgccttcgcc gtccctcgcc tcgggtcctc cgtcctcgcc caccgctccc 840
tcctcggtgg tcggcgcgac ctccggcgcc gggaggcccc gcctgggcag aggtcgaaac 900
agtaacaaag gactgcctca gtctacgatt tcttttgatg gaatctatgc aaatatgagg 960
atggttcata tacttacatc agttgttggc tccaaatgtg aagtacaagt gaaaaatgga 1020
ggtatatatg aaggagtttt taaaacttac agtccgaagt gtgatttggg acttgatgcc 1080
gcacatgaga aaagtacaga atccagttcg gggccgaaac gtgaagaaat aatggagagt 1140
atthttgttc aatgttcaga ctttgttgtg gtacagttta aagatatgga ctccagttat 1200
gcaaaaagag atgctttttac tgactctgct atcagtgcga aagtgaatgg cgaacacaaa 1260
gagaaggacc tggagccctg ggatgcaggt gaactcacag ccaatgagga acttgaggct 1320
ttggaaaatg acgtatctaa tggatgggat cccaatgata tgtttcgata taatgaagaa 1380
aattatggtg tagtgtctac gtatgatagc agtttatctt cgtatacagt gcccttagaa 1440
agagataact cagaagaatt tttaaaacgg gaagcaaggg caaaccagtt agcagaagaa 1500
attgagtcaa gtgcccagta caaagctcga gtggccctgg aaaatgatga taggagtggag 1560
gaagaaaaat acacagcagt tcagagaaat tccagtgaac gtgaggggca cagcataaac 1620
actagggaaa ataaatatat tcctcctgga caaagaaata gagaagtcac atcctggggg 1680
agtgggagac agaattcacc gcgtatgggc cagcctggat cgggctccat gccatcaaga 1740
tccacttctc acacttcaga tttcaaccgc aattctggtt cagaccaaag agtagttaat 1800
ggaggtgttc cctggccatc gccttgccca tctccttctc ctccgccacc ttctcgctac 1860
cagtcaggtc ccaactctct tccacctcgg gcagccaccc ctacacggcc gccctccagg 1920
ccccctcgc ggccatccag acccccgctc caccctctg ctcatggttc tccagctcct 1980
gtctctacta tgccataaac catgtcttca gaagggcctc caaggatgtc cccaaaggcc 2040
cagcgacatc ctcgaaatca cagagtttct gctgggaggg gttccatata cagtggccta 2100
```

gaatttgtat	cccacaaccc	acccagtgaa	gcagctactc	ctccagtagc	aaggaccagt	2160
ccctcggggg	gaacgtgggc	atcagtggtc	agtgggggtc	caagattatc	ccctaaaact	2220
catagaccca	ggtctcccag	acagaacagt	attggaaaata	ccccagtg	gccagttctt	2280
gcttctcccc	aagctgggat	tattccaact	gaagctgttg	ccatgcctat	tccagctgca	2340
tctcctacgc	ctgctagtcc	tgcacgaac	agagctgtta	ccccttctag	tgaggctaaa	2400
gattccaggc	ttcaagatca	gaggcagaac	tctcctgcag	ggaataaaga	aaatattaaa	2460
cccaatgaaa	catcacctag	cttctcaaaa	gctgaaaaca	aaggtatatc	accagttggt	2520
tctgaacata	gaaaacagat	tgatgattta	aagaaattta	agaatgattt	taggttacag	2580
ccaagttcta	cttctgaatc	tatggatcaa	ctactaaaca	aaaatagaga	gggagaaaaa	2640
tcaagagatt	tgatcaaaga	caaaattgaa	ccaagtgc	aggattcttt	cattgaaaaa	2700
agcagcagca	actgtaccag	tggcagcagc	aagccgaata	gccccagcat	ttccccttca	2760
atacttagta	acacggagca	caagagggga	cctgaggtca	cttcccaagg	ggttcagact	2820
tccagcccag	catgtaaaca	agagaaagac	gataagggaag	agaagaaaga	cgcagctgag	2880
caagttagga	aatcaacatt	gaatcccaat	gcaaaggagt	tcaaccacg	ttccttctct	2940
cagccaaagc	cttctactac	cccaacttca	cctcggcctc	aagcacaacc	tagcccatct	3000
atggtgggtc	atcaacagcc	aactccagtt	tatactcagc	ctgtttgttt	tgcaccaa	3060
atgatgtatc	cagtcccagt	gagcccaggc	gtgcaacctt	tatacccaat	acctatgacg	3120
cccagtcag	tgaatcaagc	caagacatat	agagcagtac	caaatatgcc	ccaacagcgg	3180
caagaccagc	atcatcagag	tgccatgatg	caccagcgt	cagcagcggg	cccaccgatt	3240
gcagccaccc	caccagctta	ctccacgcaa	tatgttgctt	acagtcctca	gcagttccca	3300
aatcagcccc	ttgttcagca	tgtgccacat	tatcagtctc	agcatcctca	tgtctatagt	3360
cctgtaatac	agggtaatgc	tagaatgatg	gcaccaccaa	cacacgcca	gcctggttta	3420
gtatcttctt	cagcaactca	gtacggggct	catgagcaga	cgcatgcgat	gtatgcatgt	3480
cccaaattac	catacaacaa	ggagacaagc	ccttctttct	actttgccat	ttccacgggc	3540
tcccttgctc	agcagtatgc	gcaccctaac	gctaccctgc	accacatac	tccacaccct	3600
cagccttcag	ctacccccac	tggacagcag	caaagccaac	atggtggaag	tcacctgca	3660
cccagtcctg	ttcagcacca	tcagcaccag	gccgcccagg	ctctccatct	ggccagtcca	3720
cagcagcagt	cagccattta	ccacgcgggg	cttgcgccaa	ctccaccctc	catgacacct	3780
gcctccaaca	cgcagtcgcc	acagaatagt	ttcccagcag	cacaacagac	tgtctttacg	3840
atccatcctt	ctcacgttca	gccggcgtat	accaaccac	cccacatggc	ccacgtacct	3900
caggctcatg	tacagtcagg	aatggttcct	tctcatccaa	ctgcccattg	gccaatgatg	3960
ctaatacga	cacagccacc	cggcgggtccc	caggccgccc	tcgctcaaag	tgactacag	4020
cccattccag	tctcgacaac	agcgcatttc	ccctatatga	cgcacccttc	agtacaagcc	4080
caccaccaac	agcagttgta	aggctgccct	ggaggaaaccg	aaaggccaaa	ttccctcctc	4140
ccttctactg	cttctacca	ctggaagcac	agaaaactag	aatttcattt	attttgtttt	4200
taaaatatat	atgttgattt	cttgaacat	ccaataggaa	tgctaacagt	tcacttgag	4260
tggaagatac	ttggaccgag	tagaggcatt	taggaacttg	ggggctattc	cataattcca	4320
tatgctgttt	cagagtcccg	caggtacccc	agctctgctt	gccgaaactg	gaagttattt	4380
attttttaat	aacccttgaa	agtcatgaac	acatcagcta	gcaaaagaag	taacaagagt	4440
gattcttgct	gctattactg	ctaaaaaaaa	aaaaaaaaaa	a		4481